SEQUENCE LISTING

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Burlingame, Richard P.
Millis, James R.

<120> PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE

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ctc ggt aaa gtc cag atg ctg gca cag gca gcg gaa gaa cat cct ctg   192
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His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
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Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
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gtg cat aac ggc atc atc gaa aac cat gaa ccg ctg cgt gaa gag cta   336
Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
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aaa gcg cgt ggc tat acc ttc gtt tct gaa acc gac acc gaa gtg att   384
Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
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gcc cat ctg gtg aac tgg gag ctg aaa caa ggc ggg act ctg cgt gag   432
Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
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gcc gtt ctg cgt gct atc ccg cag ctg cgt ggt gcg tac ggt aca gtg   480
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Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
305                 310                 315                 320

att ccg tgc gac gtc gaa atc gcc tct gaa ttc cgc tat cgc aaa tct   1008
Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
                325                 330                 335

gcc gtg cgt cgt aac agc ctg atg atc acc ttg tca cag tct ggc gaa   1056
Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
            340                 345                 350

acc gcg gat acc ctg gct ggc ctg cgt ctg tcg aaa gag ctg ggt tac   1104
Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
        355                 360                 365

ctt ggt tca ctg gca atc tgt aac gtt ccg ggt tct tct ctg gtg cgc   1152
Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
    370                 375                 380

gaa tcc gat ctg gcg cta atg acc aac gcg ggt aca gaa atc ggc gtg   1200
Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
385                 390                 395                 400
```

```
gca tcc act aaa gca ttc acc act cag tta act gtg ctg ttg atg ctg   1248
Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
                405                 410                 415

gtg gcg aag ctg tct cgc ctg aaa ggt ctg gat gcc tcc att gaa cat   1296
Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
            420                 425                 430

gac atc gtg cat ggt ctg cag gcg ctg ccg agc cgt att gag cag atg   1344
Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
        435                 440                 445

ctg tct cag gac aaa cgc att gaa gcg ctg gca gaa gat ttc tct gac   1392
Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
    450                 455                 460

aaa cat cac gcg ctg ttc ctg ggc cgt ggc gat cag tac cca atc gcg   1440
Lys His His Ala Leu Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala
465                 470                 475                 480

ctg gaa ggc gca ttg aag ttg aaa gag atc tct tac att cac gct gaa   1488
Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
                485                 490                 495

gcc tac gct gct ggc gaa ctg aaa cac ggt ccg ctg gcg cta att gat   1536
Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
            500                 505                 510

gcc gat atg ccg gtt att gtt gtt gca ccg aac aac gaa ttg ctg gaa   1584
Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
        515                 520                 525

aaa ctg aaa tcc aac att gaa gaa gtt cgc gcg cgt ggc ggt cag ttg   1632
Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
    530                 535                 540

tat gtc ttc gcc gat cag gat gcg ggt ttt gta agt agc gat aac atg   1680
Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545                 550                 555                 560

cac atc atc gag atg ccg cat gtg gaa gag gtg att gca ccg atc ttc   1728
His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
                565                 570                 575

tac acc gtt ccg ctg cag ctg ctg gct tac cat gtc gcg ctg atc aaa   1776
Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
            580                 585                 590
```

```
ggc acc gac gtt gac cag ccg cgt aac ctg gca aaa tcg gtt acg gtt   1824
Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
        595                 600                 605

gag taa                                                         1830
Glu
    610
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<210> 16
<211> 609
<212> PRT
<213> Escherichia coli

<400> 16

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Met Cys Gly Ile Val Gly Ala Ile Ala Gln Arg Asp Val Ala Glu Ile
  1               5                  10                  15

Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
             20                  25                  30

Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
         35                  40                  45

Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
     50                  55                  60

His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
 65                  70                  75                  80

Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
                 85                  90                  95

Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
            100                 105                 110

Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
        115                 120                 125

Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
    130                 135                 140

Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
145                 150                 155                 160

Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
                165                 170                 175
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Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
180 185 190

Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
195 200 205

Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
210 215 220

Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
225 230 235 240

Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu
245 250 255

Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
260 265 270

Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
275 280 285

Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
290 295 300

Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
305 310 315 320

Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
325 330 335

Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
340 345 350

Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
355 360 365

Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
370 375 380

Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
385 390 395 400

Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
405 410 415

Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
420 425 430

Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
435 440 445

Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
450 455 460

Lys His His Ala Leu Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala
465 470 475 480

Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
485 490 495

Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
500 505 510

Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
515 520 525

Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
530 535 540

Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545 550 555 560

His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
565 570 575

Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
580 585 590

Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
595 600 605

Glu

<210> 17
<211> 2184
<212> DNA
<213> Escherichia coli

<400> 17
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accatgtgtg gaactgttgg cgcgatcgcg caacgtgatg tagcagaaat ccttcttgaa 180

ggtttacgtc gtctggaata ccgcggatat gactctgccg gtctggccgt tgttgatgca 240

gaaggtcata tgacccgcct gcgtcgcctc ggtaaagtcc agatgctggc acaggcagcg 300

gaagaacatc ctctgcatgg cggcactggt attgctcaca ctcgctgggc gacccacggt 360

gaaccttcag aagtgaatgc gcatccgcat gtttctgaac acattgtggt ggtgcataac 420

ggcatcatcg aaaaccatga accgctgcgt gaagagctaa aagcgcgtgg ctataccttc 480

gtttctgaaa ccgacaccga agtgattgcc catctggtga actgggagct gaaacaaggc 540

gggactctgc gtgaggccgt tctgcgtgct atcccgcagc tgcgtggtgc gtacggtaca 600

gtgatcatgg actcccgtca cccggatacc ctgctggcgg cacgttctgg tagtccgctg 660

gtgattggcc tggggatggg cgaaaacttt atcgcttctg accagctggc gctgttgccg 720

gtgacccgtc gctttatctt ccttgaagag ggcgatattg cggaaatcac tcgccgttcg 780

gtaaacatct tcgataaaac tggcgcggaa gtaaaacgtc aggatatcga atccaatctg 840

caatatgacg cgggcgataa aggcatttac cgtcactaca tgcagaaaga gatctacgaa 900

cagccgaacg cgatcaaaaa cacccttacc ggacgcacca gccacggtca ggttgattta 960

agcgagctgg gaccgaacgc cgacgaactg ctgtcgaagg ttgagcatat tcagatcctc 1020

gcctgtggta cttcttataa ctccggtatg gtttcccgct actggtttga atcgctagca 1080

ggtattccgt gcgacgtcga aatcgcctct gaattccgct atcgcaaatc tgccgtgcgt 1140

cgtaacagcc tgatgatcac cttgtcacag tctggcgaaa ccgcggatac cctggctggc 1200

ctgcgtctgt cgaaagagct gggttacctt ggttcactgg caatctgtaa cgttccgggt 1260

tcttctctgg tgcgcgaatc cgatctggcg ctaatgacca acgcgggtac agaaatcggc 1320

gtggcatcca ctaaagcatt caccactcag ttaactgtgc tgttgatgct ggtggcgaag 1380

ctgtctcgcc tgaaaggtct ggatgcctcc attgaacatg acatcgtgca tggtctgcag 1440

gcgctgccga gccgtattga gcagatgctg cctcaggaca aacgcattga agcgctggca 1500

gaagatttct ctgacaaaca tcacgcgctg ttcctgggcc gtggcgatca gtacccaatc 1560

gcgctggaag gcgcattgaa gttgaaagag atctcttaca ttcacgctga agcctacgct 1620

gctggcgaac tgaaacacgg tccgctggcg ctaattgatg ccgatatgcc ggttattgtt 1680

gttgcaccga acaacgaatt gctggaaaaa ctgaaatcca acattgaaga agttcgcgcg 1740

cgtggcggtc agttgtatgt cttcgccgat caggatgcgg gttttgtaag tagcgataac 1800

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ccgctgcagc tgctggctta ccatgtcgcg ctgatcaaag gcaccgacgt tgaccagccg 1920

cgtaacctgg caaaatcggt tacggttgag taataaatgg atgccctgcg taagcggggc 1980

atttttcttc ctgttatgtt tttaatcaaa catcctgcca actccatgtg acaaaccgtc 2040

atcttcggct actttttctc tgtcacagaa tgaaaatttt tctgtcatct cttcgttatt 2100

aatgtttgta attgactgaa tatcaacgct ctagaggggc tagagcggcc gccaccgcgg 2160

tggagctccg tcgacaagct tatc 2184

<210> 18
<211> 1830
<212> DNA
<213> Escherichia coli

<220>
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<400> 18

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Met Cys Gly Thr Val Gly Ala Ile Ala Gln Arg Asp Val Ala Glu Ile
  1               5                  10                  15

ctt ctt gaa ggt tta cgt cgt ctg gaa tac cgc gga tat gac tct gcc   96
Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
             20                  25                  30

ggt ctg gcc gtt gtt gat gca gaa ggt cat atg acc cgc ctg cgt cgc   144
Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
         35                  40                  45

ctc ggt aaa gtc cag atg ctg gca cag gca gcg gaa gaa cat cct ctg   192
Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
     50                  55                  60
```

```
cat ggc ggc act ggt att gct cac act cgc tgg gcg acc cac ggt gaa   240
His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
 65                  70                  75                  80

cct tca gaa gtg aat gcg cat ccg cat gtt tct gaa cac att gtg gtg   288
Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
                 85                  90                  95

gtg cat aac ggc atc atc gaa aac cat gaa ccg ctg cgt gaa gag cta   336
Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
            100                 105                 110

aaa gcg cgt ggc tat acc ttc gtt tct gaa acc gac acc gaa gtg att   384
Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
        115                 120                 125

gcc cat ctg gtg aac tgg gag ctg aaa caa ggc ggg act ctg cgt gag   432
Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
    130                 135                 140

gcc gtt ctg cgt gct atc ccg cag ctg cgt ggt gcg tac ggt aca gtg   480
Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
145                 150                 155                 160

atc atg gac tcc cgt cac ccg gat acc ctg ctg gcg gca cgt tct ggt   528
Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
                165                 170                 175

agt ccg ctg gtg att ggc ctg ggg atg ggc gaa aac ttt atc gct tct   576
Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
            180                 185                 190

gac cag ctg gcg ctg ttg ccg gtg acc cgt cgc ttt atc ttc ctt gaa   624
Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
        195                 200                 205

gag ggc gat att gcg gaa atc act cgc cgt tcg gta aac atc ttc gat   672
Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
    210                 215                 220

aaa act ggc gcg gaa gta aaa cgt cag gat atc gaa tcc aat ctg caa   720
Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
225                 230                 235                 240

tat gac gcg ggc gat aaa ggc att tac cgt cac tac atg cag aaa gag   768
Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu
                245                 250                 255
```

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atc tac gaa cag ccg aac gcg atc aaa aac acc ctt acc gga cgc acc   816
Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Thr
            260                 265                 270

agc cac ggt cag gtt gat tta agc gag ctg gga ccg aac gcc gac gaa   864
Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
        275                 280                 285

ctg ctg tcg aag gtt gag cat att cag atc ctc gcc tgt ggt act tct   912
Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
    290                 295                 300

tat aac tcc ggt atg gtt tcc cgc tac tgg ttt gaa tcg cta gca ggt   960
Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
305                 310                 315                 320

att ccg tgc gac gtc gaa atc gcc tct gaa ttc cgc tat cgc aaa tct   1008
Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
                325                 330                 335

gcc gtg cgt cgt aac agc ctg atg atc acc ttg tca cag tct ggc gaa   1056
Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
        340                 345                 350

acc gcg gat acc ctg gct ggc ctg cgt ctg tcg aaa gag ctg ggt tac   1104
Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
        355                 360                 365

ctt ggt tca ctg gca atc tgt aac gtt ccg ggt tct tct ctg gtg cgc   1152
Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
    370                 375                 380

gaa tcc gat ctg gcg cta atg acc aac gcg ggt aca gaa atc ggc gtg   1200
Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
385                 390                 395                 400

gca tcc act aaa gca ttc acc act cag tta act gtg ctg ttg atg ctg   1248
Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
                405                 410                 415

gtg gcg aag ctg tct cgc ctg aaa ggt ctg gat gcc tcc att gaa cat   1296
Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
            420                 425                 430

gac atc gtg cat ggt ctg cag gcg ctg ccg agc cgt att gag cag atg   1344
Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
        435                 440                 445
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```
ctg cct cag gac aaa cgc att gaa gcg ctg gca gaa gat ttc tct gac   1392
Leu Pro Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
    450                 455                 460

aaa cat cac gcg ctg ttc ctg ggc cgt ggc gat cag tac cca atc gcg   1440
Lys His His Ala Leu Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala
465                 470                 475                 480

ctg gaa ggc gca ttg aag ttg aaa gag atc tct tac att cac gct gaa   1488
Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
                485                 490                 495

gcc tac gct gct ggc gaa ctg aaa cac ggt ccg ctg gcg cta att gat   1536
Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
            500                 505                 510

gcc gat atg ccg gtt att gtt gtt gca ccg aac aac gaa ttg ctg gaa   1584
Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
        515                 520                 525

aaa ctg aaa tcc aac att gaa gaa gtt cgc gcg cgt ggc ggt cag ttg   1632
Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
    530                 535                 540

tat gtc ttc gcc gat cag gat gcg ggt ttt gta agt agc gat aac atg   1680
Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545                 550                 555                 560

cac atc atc gag atg ccg cat gtg gaa gag gtg att gca ccg atc ttc   1728
His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
                565                 570                 575

tac acc gtt ccg ctg cag ctg ctg gct tac cat gtc gcg ctg atc aaa   1776
Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
            580                 585                 590

ggc acc gac gtt gac cag ccg cgt aac ctg gca aaa tcg gtt acg gtt   1824
Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
        595                 600                 605

gag taa                                                         1830
Glu
    610
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<210> 19
<211> 609
<212> PRT

<213> Escherichia coli

<400> 19

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Met Cys Gly Thr Val Gly Ala Ile Ala Gln Arg Asp Val Ala Glu Ile
  1               5                  10                  15

Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
             20                  25                  30

Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
         35                  40                  45

Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
     50                  55                  60

His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
 65                  70                  75                  80

Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
                 85                  90                  95

Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
            100                 105                 110

Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
        115                 120                 125

Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
    130                 135                 140

Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
145                 150                 155                 160

Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
                165                 170                 175

Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
            180                 185                 190

Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
        195                 200                 205

Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
    210                 215                 220

Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
225                 230                 235                 240
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Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu
245 250 255

Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Thr
260 265 270

Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
275 280 285

Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
290 295 300

Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
305 310 315 320

Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
325 330 335

Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
340 345 350

Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
355 360 365

Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
370 375 380

Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
385 390 395 400

Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
405 410 415

Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
420 425 430

Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
435 440 445

Leu Pro Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
450 455 460

Lys His His Ala Leu Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala
465 470 475 480

Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
485 490 495

Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
500 505 510

Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
515 520 525

Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
530 535 540

Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545 550 555 560

His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
565 570 575

Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
580 585 590

Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
595 600 605

Glu

<210> 20
<211> 2184
<212> DNA
<213> Escherichia coli

<400> 20
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accatgtgtg gaattgttgg cgcgatcgcg caacgtgatg tagcagaaat ccttcttgaa 180

ggtttacgtc gtctggaata ccgcggatat gactctgccg gtctggccgt tgttgataca 240

gaaggtcata tgacccgcct gcgtcgcctc ggtaaagtcc agatgctggc acaggcagcg 300

gaagaacatc ctctgcatgg cggcactggt attgctcaca ctcgctgggc gacccacggt 360

gaaccttcag aagtgaatgc gcatccgcat gtttctgaac acattgtggt ggtgcataac 420

ggcatcatcg aaaaccatga accgctgcgt gaagagctaa aagcgcgtgg ctataccttc 480

gtttctgaaa ccgacaccga agtgattgcc catctggtga actgggagct gaaacaaggc 540

gggactctgc gtgaggccgt tctgcgtgct atcccgcagc tgcgtggtgc gtacggtaca 600

gtgatcatgg actcccgtca cccggatacc ctgctggcgg cacgttctgg tagtccgctg 660

gtgattggcc tggggatggg cgaaaacttt atcgcttctg accagctggc gctgttgccg 720

gtgacccgtc gctttatctt ccttgaagag ggcgatattg cggaaatcac tcgccgttcg 780

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caatatgacg cgggcgataa aggcatttac tgtcactaca tgcagaaaga gatctacgaa 900

cagccgaacg cgatcaaaaa cacccttacc ggacgcatca gccacggtca ggttgattta 960

agcgagctgg gaccgaacgc cgacgaactg ctgtcgaagg ttgagcatat tcagatcctc 1020

gcctgtggta cttcttataa ctccggtatg gtttcccgct actggtttga atcgctagca 1080

ggtattccgt gcgacgtcga aatcgcctcc gaattccgct atcgcaaatc tgccgtgcgt 1140

cgtaacagcc tgatgatcac cttgtcacag tctggcgaaa ccgcggatac cctggctggc 1200

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  1               5                  10                  15

ctt ctt gaa ggt tta cgt cgt ctg gaa tac cgc gga tat gac tct gcc   96
Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
             20                  25                  30

ggt ctg gcc gtt gtt gat aca gaa ggt cat atg acc cgc ctg cgt cgc   144
Gly Leu Ala Val Val Asp Thr Glu Gly His Met Thr Arg Leu Arg Arg
         35                  40                  45

ctc ggt aaa gtc cag atg ctg gca cag gca gcg gaa gaa cat cct ctg   192
Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
     50                  55                  60

cat ggc ggc act ggt att gct cac act cgc tgg gcg acc cac ggt gaa   240
His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
 65                  70                  75                  80

cct tca gaa gtg aat gcg cat ccg cat gtt tct gaa cac att gtg gtg   288
Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
                 85                  90                  95

gtg cat aac ggc atc atc gaa aac cat gaa ccg ctg cgt gaa gag cta   336
Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
            100                 105                 110

aaa gcg cgt ggc tat acc ttc gtt tct gaa acc gac acc gaa gtg att   384
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Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
        115                 120                 125

gcc cat ctg gtg aac tgg gag ctg aaa caa ggc ggg act ctg cgt gag   432
Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
    130                 135                 140

gcc gtt ctg cgt gct atc ccg cag ctg cgt ggt gcg tac ggt aca gtg   480
Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
145                 150                 155                 160

atc atg gac tcc cgt cac ccg gat acc ctg ctg gcg gca cgt tct ggt   528
Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
                165                 170                 175

agt ccg ctg gtg att ggc ctg ggg atg ggc gaa aac ttt atc gct tct   576
Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
            180                 185                 190

gac cag ctg gcg ctg ttg ccg gtg acc cgt cgc ttt atc ttc ctt gaa   624
Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
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gag ggc gat att gcg gaa atc act cgc cgt tcg gta aac atc ttc gat   672
Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
    210                 215                 220

aaa act ggc gcg gaa gta aaa cgt cag gat atc gaa tcc aat ctg caa   720
Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
225                 230                 235                 240

tat gac gcg ggc gat aaa ggc att tac tgt cac tac atg cag aaa gag   768
Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Cys His Tyr Met Gln Lys Glu
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atc tac gaa cag ccg aac gcg atc aaa aac acc ctt acc gga cgc atc   816
Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
            260                 265                 270

agc cac ggt cag gtt gat tta agc gag ctg gga ccg aac gcc gac gaa   864
Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
        275                 280                 285

ctg ctg tcg aag gtt gag cat att cag atc ctc gcc tgt ggt act tct   912
Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
    290                 295                 300

tat aac tcc ggt atg gtt tcc cgc tac tgg ttt gaa tcg cta gca ggt   960
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Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
305                 310                 315                 320

att ccg tgc gac gtc gaa atc gcc tcc gaa ttc cgc tat cgc aaa tct   1008
Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
                325                 330                 335

gcc gtg cgt cgt aac agc ctg atg atc acc ttg tca cag tct ggc gaa   1056
Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
            340                 345                 350

acc gcg gat acc ctg gct ggc ctg cgt ctg tcg aaa gag ctg ggt tac   1104
Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
        355                 360                 365

ctt ggt tca ctg gca atc tgt aac gtt ccg ggt tct tct ctg gtg cgc   1152
Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
    370                 375                 380

gaa tcc gat ctg gcg cta atg acc aac gcg ggt aca gaa atc ggc gtg   1200
Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
385                 390                 395                 400

gca tcc act aaa gca ttc acc act cag tta act gtg ctg ttg atg ctg   1248
Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
                405                 410                 415

gtg gcg aag ctg tct cgc ctg aaa ggt ctg gat gcc tcc att gaa cat   1296
Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
            420                 425                 430

gac atc gtg cat ggt ctg cag gcg ctg ccg agc cgt att gag cag atg   1344
Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
        435                 440                 445

ctg tct cag gac aaa cgc att gaa gcg ctg gca gaa gat ttc tct gac   1392
Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
    450                 455                 460

aaa cat cac gcg ctg ttc ctg agc cgt ggc gat cag tac cca atc gcg   1440
Lys His His Ala Leu Phe Leu Ser Arg Gly Asp Gln Tyr Pro Ile Ala
465                 470                 475                 480

ctg gaa ggc gca ttg aag ttg aaa gag atc tct tac att cac gct gaa   1488
Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
                485                 490                 495

gcc tac gct gct ggc gaa ctg aaa cac ggt ccg ctg gcg cta att gat   1536
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Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
500 505 510

gcc gat atg ccg gtt att gtt gtt gca ccg aac aac gaa ttg ctg gaa 1584
Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
515 520 525

aaa ctg aaa tcc aac att gaa gaa gtt cgc gcg cgt ggc ggt cag ttg 1632
Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
530 535 540

tat gtc ttc gcc gat cag gat gcg ggt ttt gta agt agc gat aac atg 1680
Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545 550 555 560

cac atc atc gag atg ccg cat gtg gaa gag gtg att gca ccg atc ttc 1728
His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
565 570 575

tac acc gtt ccg ctg cag ctg ctg gct tac cat gtc gcg ctg atc aaa 1776
Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
580 585 590

ggc acc gac gtt gac cag ccg cgt aac ctg gca aaa tcg gtt acg gtt 1824
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595 600 605

gag taa 1830
Glu
610

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35 40 45

Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu

50 55 60

His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
65 70 75 80

Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
85 90 95

Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
100 105 110

Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
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Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
130 135 140

Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
145 150 155 160

Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
165 170 175

Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
180 185 190

Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
195 200 205

Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
210 215 220

Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
225 230 235 240

Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Cys His Tyr Met Gln Lys Glu
245 250 255

Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
260 265 270

Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
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Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
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Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly

305 310 315 320

Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
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Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
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Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
370 375 380

Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
385 390 395 400

Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
405 410 415

Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
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Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
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Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
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Lys His His Ala Leu Phe Leu Ser Arg Gly Asp Gln Tyr Pro Ile Ala
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Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
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Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
500 505 510

Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
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Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
530 535 540

Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545 550 555 560

His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe

565 570 575

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20 25 30

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Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
35 40 45

ctc ggt aaa gtc cag atg ctg gca cag gca gcg gaa gaa cat cct ctg 192
Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
50 55 60

cat ggc ggc act ggt att gct cac act cgc tgg gcg acc cac ggt gaa 240
His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
65 70 75 80

cct tca gaa gtg aat gcg cat ccg cat gtt tcc gaa cac att gtg gtg 288
Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
85 90 95

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Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
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Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
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Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly

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Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
            180                 185                 190

gac cag ctg gcg ctg ttg ccg gtg acc cgt cgc ttt atc ttc ctt gaa   624
Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
        195                 200                 205

gag ggc gat att gcg gaa atc act cgc cgt tcg gta aac atc ttc gat   672
Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
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aaa act ggc gcg gaa gta aaa cgt cag gat atc gaa tcc aat ctg caa   720
Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
225                 230                 235                 240

tat gac gcg ggc gat aaa ggc att tac cgt cac tac atg cag aaa gag   768
Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu
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atc tac gaa cag ccg aac gcg atc aaa aac acc ctt acc gga cgc atc   816
Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
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agc cac ggt cag gtt gat tta agc gag ctg gga ccg aac gcc gac gaa   864
Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
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ctg ctg tcg aag gtt gag cat att cag atc ctc gcc tgt ggt act tct   912
Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
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Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
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att ccg tgc gac gtc gaa atc gcc tct gaa ttc cgc tat cgc aaa tct  1008
Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
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gcc gtg cgt cgt aac agc ctg atg atc acc ttg tca cag tct ggc gaa  1056
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385                 390                 395                 400

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aaa cat cac gcg ccg ttc ctg ggc cgt ggc gat cag tac cca atc gcg   1440
Lys His His Ala Pro Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala
465                 470                 475                 480

ctg gaa ggc gca ttg aag ttg aaa gag atc tct tac att cac gct gaa   1488
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                485                 490                 495

gcc tac gct gct ggc gaa ctg aaa cac ggt ccg ctg gcg cta att gat   1536
Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
            500                 505                 510

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Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
        515                 520                 525

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    530                 535                 540

tat gtc ttc gcc gat cag gat gcg ggt ttt gta agt agc gat aac atg   1680
Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
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565 570 575

tac acc gtt ccg ctg cag ctg ctg gct tac cat gtc gcg ctg atc aaa 1776
Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
580 585 590

ggc acc gac gtt gac cag ccg cgt aac ctg gca aaa tcg gtt acg gtt 1824
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595 600 605

gag taa 1830
Glu
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20 25 30

Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
35 40 45

Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
50 55 60

His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
65 70 75 80

Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
85 90 95

Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
100 105 110

Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
115 120 125

Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
130 135 140

Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
145 150 155 160

Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
165 170 175

Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
180 185 190

Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
195 200 205

Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
210 215 220

Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
225 230 235 240

Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu
245 250 255

Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
260 265 270

Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
275 280 285

Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
290 295 300

Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
305 310 315 320

Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
325 330 335

Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
340 345 350

Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
355 360 365

Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
370 375 380

Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
385 390 395 400

Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
405 410 415

Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
420 425 430

Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
435 440 445

Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
450 455 460

Lys His His Ala Pro Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala
465 470 475 480

Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
485 490 495

Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
500 505 510

Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
515 520 525

Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
530 535 540

Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545 550 555 560

His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
565 570 575

Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
580 585 590

Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
595 600 605

Glu

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<211> 2184

<212> DNA
<213> Escherichia coli

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accatgtgtg gaattgttgg cgcgatcgcg caacgtgatg tagcagaaat ccttcttgaa 180

ggtttacgtc gtctggaata ccgcggatat gactctgccg gtctggccgt tgttgatgca 240

gaaggtcata tgacccgcct gcgtcgcctc ggtaaagtcc agatgctggc acaggcagcg 300

gaagaacatc ctctgcatgg cggcactggt attgctcaca ctcgctgggc gacccacggt 360

gaaccttcag aagtgaatgc gcatccgcat gtttctgaac acattgtggt ggtgcataac 420

ggcatcatcg aaaaccatga accgctgcgt gaagagctaa aagcgcgtgg ctataccttc 480

gtttctgaaa ccgacaccga agtgattgcc catctggtga actgggagct gaaacaaggc 540

gggactctgc gtgaggccgt tctgcgtgct atcccgcagc tgcgtggtgc gtacggtaca 600

gtgatcatgg actcccgtca cccggatacc ctgctggcgg cacgttctgg tagtccgctg 660

gtgattggcc tggggatggg cgaaaacttt atcgcttctg accagctggc gctgttgccg 720

gtgacccgtc gctttatctt ccttgaagag ggcgatattg cggaaatcac tcgccgttcg 780

gtaaacatct tcgataaaac tggcgcggaa gtaaaacgtc aggatatcga atccaatctg 840

caatatgacg cgggcgataa aggcatttac cgtcactaca tgcagaaaga gatctacgaa 900

cagccgaacg cgatcaaaaa cacccttacc ggacgcatca gccacggtca ggttgattta 960

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gcctgtggta cttcttataa ctccggtatg gtttcccgct actggtttga atcgctagca 1080

ggtattccgt gcgacgtcga aatcgcctct gaattccgct atcgcaaatc tgccgtgcgt 1140

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ctgtctcgcc tgaaaggtct ggatgcctcc attgaacatg acatcgtgca tggtctgcag 1440

gcgctgccga gccgtattga gcagatgctg tctcaggaca aacgcattga agcgctggca 1500

gaagatttct ctgacaaaca tcacgcgctg ttcctgagcc gtggcgatca gtacccaatc 1560

gcgctggaag gcgcattgaa gttgaaagag atctcttaca ttcacgctga agcctacgct 1620

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atttttcttc ctgttatgtt tttaatcaaa catcctgcca actccatgtg acaaaccgtc 2040

atcttcggct actttttctc tgtcacagaa tgaaaatttt tctgtcatct cttcgttatt 2100

aatgtttgta attgactgaa tatcaacgct ctaggggggc tagagcggcc gccaccgcgg 2160

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<211> 1830
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<220>
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1 5 10 15

ctt ctt gaa ggt tta cgt cgt ctg gaa tac cgc gga tat gac tct gcc 96
Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
20 25 30

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ggt ctg gcc gtt gtt gat gca gaa ggt cat atg acc cgc ctg cgt cgc   144
Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
         35                  40                  45

ctc ggt aaa gtc cag atg ctg gca cag gca gcg gaa gaa cat cct ctg   192
Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
     50                  55                  60

cat ggc ggc act ggt att gct cac act cgc tgg gcg acc cac ggt gaa   240
His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
 65                  70                  75                  80

cct tca gaa gtg aat gcg cat ccg cat gtt tct gaa cac att gtg gtg   288
Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
                 85                  90                  95

gtg cat aac ggc atc atc gaa aac cat gaa ccg ctg cgt gaa gag cta   336
Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
            100                 105                 110

aaa gcg cgt ggc tat acc ttc gtt tct gaa acc gac acc gaa gtg att   384
Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
        115                 120                 125

gcc cat ctg gtg aac tgg gag ctg aaa caa ggc ggg act ctg cgt gag   432
Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
    130                 135                 140

gcc gtt ctg cgt gct atc ccg cag ctg cgt ggt gcg tac ggt aca gtg   480
Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
145                 150                 155                 160

atc atg gac tcc cgt cac ccg gat acc ctg ctg gcg gca cgt tct ggt   528
Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
                165                 170                 175

agt ccg ctg gtg att ggc ctg ggg atg ggc gaa aac ttt atc gct tct   576
Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
            180                 185                 190

gac cag ctg gcg ctg ttg ccg gtg acc cgt cgc ttt atc ttc ctt gaa   624
Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
        195                 200                 205

gag ggc gat att gcg gaa atc act cgc cgt tcg gta aac atc ttc gat   672
Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
    210                 215                 220
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aaa act ggc gcg gaa gta aaa cgt cag gat atc gaa tcc aat ctg caa   720
Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
225                 230                 235                 240

tat gac gcg ggc gat aaa ggc att tac cgt cac tac atg cag aaa gag   768
Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu
                245                 250                 255

atc tac gaa cag ccg aac gcg atc aaa aac acc ctt acc gga cgc atc   816
Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
            260                 265                 270

agc cac ggt cag gtt gat tta agc gag ctg gga ccg aac gcc gac gaa   864
Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
        275                 280                 285

ctg ctg tcg aag gtt gag cat att cag atc ctc gcc tgt ggt act tct   912
Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
    290                 295                 300

tat aac tcc ggt atg gtt tcc cgc tac tgg ttt gaa tcg cta gca ggt   960
Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
305                 310                 315                 320

att ccg tgc gac gtc gaa atc gcc tct gaa ttc cgc tat cgc aaa tct   1008
Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
                325                 330                 335

gcc gtg cgt cgt aac agc ctg atg atc acc ttg tca cag tct ggc gaa   1056
Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
            340                 345                 350

acc gcg gat acc ctg gct ggc ctg cgt ctg tcg aaa gag ctg ggt tac   1104
Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
        355                 360                 365

ctt ggt tca ctg gca atc tgt aac gtt ccg ggt tct tct ctg gtg cgc   1152
Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
    370                 375                 380

gaa tcc gat ctg gcg cta atg acc aac gcg ggt aca gaa atc ggc gtg   1200
Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
385                 390                 395                 400

gca tcc act aaa gca ttc acc act cag tta act gtg ctg ttg atg ctg   1248
Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
                405                 410                 415
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gtg gcg aag ctg tct cgc ctg aaa ggt ctg gat gcc tcc att gaa cat   1296
Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
            420                 425                 430

gac atc gtg cat ggt ctg cag gcg ctg ccg agc cgt att gag cag atg   1344
Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
        435                 440                 445

ctg tct cag gac aaa cgc att gaa gcg ctg gca gaa gat ttc tct gac   1392
Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
    450                 455                 460

aaa cat cac gcg ctg ttc ctg agc cgt ggc gat cag tac cca atc gcg   1440
Lys His His Ala Leu Phe Leu Ser Arg Gly Asp Gln Tyr Pro Ile Ala
465                 470                 475                 480

ctg gaa ggc gca ttg aag ttg aaa gag atc tct tac att cac gct gaa   1488
Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
                485                 490                 495

gcc tac gct gct ggc gaa ctg aaa cac ggt ccg ctg gcg cta att gat   1536
Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
            500                 505                 510

gcc gat atg ccg gtt att gtt gtt gca ccg aac aac gaa ttg ctg gaa   1584
Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
        515                 520                 525

aaa ctg aaa tcc aac att gaa gaa gtt cgc gcg cgt ggc ggt cag ttg   1632
Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
    530                 535                 540

tat gtc ttc gcc gat cag gat gcg ggt ttt gta agt agc gat aac atg   1680
Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545                 550                 555                 560

cac atc atc gag atg ccg cat gtg gaa gag gtg att gca ccg atc ttc   1728
His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
                565                 570                 575

tac acc gtt ccg ctg cag ctg ctg gct tac cat gtc gcg ctg atc aaa   1776
Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
            580                 585                 590

ggc acc gac gtt gac cag ccg cgt aac ctg gca aaa tcg gtt acg gtt   1824
Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
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Glu
610

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<211> 609
<212> PRT
<213> Escherichia coli

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Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
20 25 30

Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
35 40 45

Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
50 55 60

His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
65 70 75 80

Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
85 90 95

Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
100 105 110

Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
115 120 125

Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
130 135 140

Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
145 150 155 160

Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
165 170 175

Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
180 185 190

Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
195 200 205

Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
210 215 220

Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
225 230 235 240

Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu
245 250 255

Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
260 265 270

Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
275 280 285

Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
290 295 300

Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
305 310 315 320

Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
325 330 335

Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
340 345 350

Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
355 360 365

Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
370 375 380

Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
385 390 395 400

Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
405 410 415

Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
420 425 430

Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
435 440 445

Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
450 455 460

Lys His His Ala Leu Phe Leu Ser Arg Gly Asp Gln Tyr Pro Ile Ala
465 470 475 480

Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
485 490 495

Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
500 505 510

Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
515 520 525

Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
530 535 540

Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545 550 555 560

His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
565 570 575

Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
580 585 590

Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
595 600 605

Glu

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<211> 2184
<212> DNA
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accatgtgtg gaattgttgg cgcgatcgcg caacgtgatg tagcagaaat ccttcttgaa 180

ggtttacgtc gtctggaata ccgcggatat gactctgccg gtctggccgt tgttgatgca 240

gaaggtcata tgacccgcct gcgtcgcctc ggtaaagtcc agatgctggc acaggcagcg 300

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gaaccttcag aagtgaatgc gcatccgcat gtttctgaac acattgtggt ggtgcataac 420

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gtttctgaaa ccgacaccga agtgattgcc catctggtga actgggagct gaaacaaggc 540

gggactctgc gtgaggccgt tctgcgtgct atcccgcagc tgcgtggtgc gtacggtaca 600

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gcgctggaag gcgcattgaa gttgaaagag atctcttaca ttcacgctga agcctacgct 1620

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atttttcttc ctgttatgtt tttaatcaaa catcctgcca actccatgtg acaaaccgtc 2040

atcttcggct actttttctc tgtcacagaa tgaaaatttt tctgtcatct cttcgttatt 2100

aatgtttgta attgactgaa tatcaacgct ctaggggggc tagagcggcc gccaccgcgg 2160

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<220>
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<400> 30

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  1               5                  10                  15

ctt ctt gaa ggt tta cgt cgt ctg gaa tac cgc gga tat gac tct gcc   96
Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
             20                  25                  30

ggt ctg gcc gtt gtt gat gca gaa ggt cat atg acc cgc ctg cgt cgc   144
Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
         35                  40                  45

ctc ggt aaa gtc cag atg ctg gca cag gca gcg gaa gaa cat cct ctg   192
Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
     50                  55                  60

cat ggc ggc act ggt att gct cac act cgc tgg gcg acc cac ggt gaa   240
His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
 65                  70                  75                  80
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cct tca gaa gtg aat gcg cat ccg cat gtt tct gaa cac att gtg gtg   288
Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
                 85                  90                  95

gtg cat aac ggc atc atc gaa aac cat gaa ccg ctg cgt gaa gag cta   336
Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
            100                 105                 110

aaa gcg cgt ggc tat acc ttc gtt tct gaa acc gac acc gaa gtg att   384
Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
        115                 120                 125

gcc cat ctg gtg aac tgg gag ctg aaa caa ggc ggg act ctg cgt gag   432
Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
    130                 135                 140

gcc gtt ctg cgt gct atc ccg cag ctg cgt ggt gcg tac ggt aca gtg   480
Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
145                 150                 155                 160

atc atg gac tcc cgt cac ccg gat acc ctg ctg gcg gca cgt tct ggt   528
Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
                165                 170                 175

agt ccg ctg gtg att ggc ctg ggg atg ggc gaa aac ttt atc gct tct   576
Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
            180                 185                 190

gac cag ctg gcg ctg ttg ccg gtg acc cgt cgc ttt atc ttc ctt gaa   624
Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
        195                 200                 205

gag ggc gat att gcg gaa atc act cgc cgt tcg gta aac atc ttc gat   672
Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
    210                 215                 220

aaa act ggc gcg gaa gta aaa cgt cag gat atc gaa tcc aat ctg caa   720
Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
225                 230                 235                 240

tat gac gcg ggc gat aaa ggc att tac cgt cac tac atg cag aaa gag   768
Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu
                245                 250                 255

atc tac gaa cag ccg aac gcg atc aaa aac acc ctt acc gga cgc atc   816
Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
            260                 265                 270
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agc cac ggt cag gtt gat tta agc gag ctg gga ccg aac gcc gac gaa   864
Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
        275                 280                 285

ctg ctg tcg aag gtt gag cat att cag atc ctc gcc tgt ggt act tct   912
Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
    290                 295                 300

tat aac tcc ggt atg gtt tcc cgc tac tgg ttt gaa tcg cta gca ggt   960
Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
305                 310                 315                 320

att ccg tgc gac gtc gaa atc gcc tct gaa ttc cgc tat cgc aaa tct   1008
Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
                325                 330                 335

gcc gtg cgt cgt aac agc ctg atg atc acc ttg tca cag tct ggc gaa   1056
Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
            340                 345                 350

acc gcg gat acc ctg gct ggc ctg cgt ctg tcg aaa gag ctg ggt tac   1104
Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
        355                 360                 365

ctt ggt tca ctg gca atc tgt aac gtt ccg ggt tct tct ctg gtg cgc   1152
Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
    370                 375                 380

gaa tcc gat ctg gcg cta atg acc aac gcg ggt aca gaa atc ggc gtg   1200
Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
385                 390                 395                 400

gca tcc act aaa gca ttc acc act cag tta act gtg ctg ttg atg ctg   1248
Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
                405                 410                 415

gtg gcg aag ctg tct cgc ctg aaa ggt ctg gat gcc tcc att gaa cat   1296
Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
            420                 425                 430

gac atc gtg cat ggt ctg cag gcg ctg ccg agc cgt att gag cag atg   1344
Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
        435                 440                 445

ctg tct cag gac aaa cgc att gaa gcg ctg gca gaa gat ttc tct gac   1392
Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
    450                 455                 460
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aaa cat cac gcg ctg ttc ctg agc cgt ggc gat cag tac cca atc gcg 1440
Lys His His Ala Leu Phe Leu Ser Arg Gly Asp Gln Tyr Pro Ile Ala
465 470 475 480

ctg gaa ggc gca ttg aag ttg aaa gag atc tct tac att cac gct gaa 1488
Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
485 490 495

gcc tac gct gct ggc gaa ctg aaa cac ggt ccg ctg gcg cta att gat 1536
Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
500 505 510

gcc gat atg ccg gtt att gtt gtt gca ccg aac aac gaa ttg ctg gaa 1584
Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
515 520 525

aaa ctg aaa tcc aac att gaa gaa gtt cgc gcg cgt ggc ggt cag ttg 1632
Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
530 535 540

tat gtc ttc gcc gat cag gat gcg ggt ttt gta agt agc gat aac atg 1680
Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
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cac atc atc gag atg ccg cat gtg gaa gag gtg att gca ccg atc ttc 1728
His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
565 570 575

tac acc gtt ccg ctg cag ctg ctg gct tac cat gtc gcg ctg atc aaa 1776
Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
580 585 590

ggc acc gac gtt gac cag ccg cgt aac ctg gca aaa tcg gtt acg gtt 1824
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595 600 605

gag taa 1830
Glu
610

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Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
35 40 45

Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
50 55 60

His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
65 70 75 80

Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
85 90 95

Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
100 105 110

Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
115 120 125

Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
130 135 140

Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
145 150 155 160

Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
165 170 175

Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
180 185 190

Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
195 200 205

Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
210 215 220

Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
225 230 235 240

Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu
245 250 255

Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile

260 265 270

Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
275 280 285

Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
290 295 300

Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
305 310 315 320

Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
325 330 335

Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
340 345 350

Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
355 360 365

Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
370 375 380

Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
385 390 395 400

Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
405 410 415

Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
420 425 430

Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
435 440 445

Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
450 455 460

Lys His His Ala Leu Phe Leu Ser Arg Gly Asp Gln Tyr Pro Ile Ala
465 470 475 480

Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
485 490 495

Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
500 505 510

Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu

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        515                 520                 525

Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
    530                 535                 540

Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545                 550                 555                 560

His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
                565                 570                 575

Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
            580                 585                 590

Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
        595                 600                 605

Glu
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